

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING

ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/566,944
Source: IFWP
Date Processed by STIC: 02/14/2006

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

SERIAL NUMBER: 10/566,944

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- | | |
|----------|--|
| 1 _____ | <p>Wrapped Nucleic
Acid Sequences</p> <p>The number/text at the end of each line "wrapped" around the line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."</p> |
| 2 _____ | <p>Invalid Line Length</p> <p>The rules require that a line not exceed 72 characters in length. This includes white spaces.</p> |
| 3 _____ | <p>Misaligned Amino
Acid Numbering</p> <p>The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.</p> |
| 4 _____ | <p>Non-ASCII</p> <p>The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.</p> |
| 5 _____ | <p>Variable Length</p> <p>Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.</p> |
| 6 _____ | <p>PatentIn 2.0
"bug"</p> <p>A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.</p> |
| 7 _____ | <p>Skipped Sequences
(OLD RULES)</p> <p>Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped</p> <p>Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.</p> |
| 8 _____ | <p>Skipped Sequences
(NEW RULES)</p> <p>Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000</p> |
| 9 _____ | <p>Use of n's or Xaa's
(NEW RULES)</p> <p><u>Use of n's and/or Xaa's have been detected in the Sequence Listing.</u>
<u>Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.</u>
<u>In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.</u></p> |
| 10 _____ | <p>Invalid <213>
Response</p> <p>Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence</p> |
| 11 _____ | <p>Use of <220></p> <p>Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)</p> |
| 12 _____ | <p>PatentIn 2.0
"bug"</p> <p>Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.</p> |
| 13 _____ | <p>Misuse of n/Xaa</p> <p>"n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid</p> |



IFWP

RAW SEQUENCE LISTING

DATE: 02/14/2006

PATENT APPLICATION: US/10/566,944

TIME: 12:55:17

Input Set : F:\Sequence listing (12810-00193-US).txt

Output Set: N:\CRF4\02142006\J566944.raw

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3 <110> APPLICANT: Zank, Thorsten
4     Bauer, Jorg
5     Cirpus, Petra
6     Abbadi, Amine
7     Heinz, Ernst
8     Qiu, Xiao
9     Vrinten, Patricia
10    Sperling, Petra
11    Domergue, Frederic
12    Meyer, Astrid
13    Kirsch, Jelena
15 <120> TITLE OF INVENTION: METHOD FOR THE PRODUCTION OF MULTIPLE-UNSATURATED FATTY
ACIDS IN
16    TRANSGENIC ORGANISMS
18 <130> FILE REFERENCE: 12810-00193-US
C--> 20 <140> CURRENT APPLICATION NUMBER: US/10/566,944
C--> 20 <141> CURRENT FILING DATE: 2006-02-01
20 <150> PRIOR APPLICATION NUMBER: DE 103 35 992.3
21 <151> PRIOR FILING DATE: 2003-08-01
23 <150> PRIOR APPLICATION NUMBER: DE 103 44 557.9
24 <151> PRIOR FILING DATE: 2003-09-24
26 <150> PRIOR APPLICATION NUMBER: DE 103 47 869.8
27 <151> PRIOR FILING DATE: 2003-10-10
29 <150> PRIOR APPLICATION NUMBER: DE 103 59 593.7
30 <151> PRIOR FILING DATE: 2003-12-18
32 <150> PRIOR APPLICATION NUMBER: DE 10 2004 009 457.8
33 <151> PRIOR FILING DATE: 2004-02-27
35 <150> PRIOR APPLICATION NUMBER: DE 10 2004 012 370.5
36 <151> PRIOR FILING DATE: 2004-03-13
38 <150> PRIOR APPLICATION NUMBER: DE 10 2004 024 014.0
39 <151> PRIOR FILING DATE: 2004-05-14
41 <160> NUMBER OF SEQ ID NOS: 192
43 <170> SOFTWARE: PatentIn version 3.1
46 <210> SEQ ID NO: 1
47 <211> LENGTH: 1266
48 <212> TYPE: DNA
49 <213> ORGANISM: Euglena gracilis
51 <220> FEATURE:
52 <221> NAME/KEY: CDS
53 <222> LOCATION: (1)..(1266)
54 <223> OTHER INFORMATION: delta8-desaturase
56 <400> SEQUENCE: 1
57 atg aag tca aag cgc caa gcg ctt ccc ctt aca att gat gga aca aca      48
58 Met Lys Ser Lys Arg Gln Ala Leu Pro Leu Thr Ile Asp Gly Thr Thr

```

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Output Set: N:\CRF4\02142006\J566944.raw

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59 1          5          10          15
61 tat gat gtg tct gcc tgg gtc aat ttc cac cct ggt ggt gcg gaa att      96
62 Tyr Asp Val Ser Ala Trp Val Asn Phe His Pro Gly Gly Ala Glu Ile
63          20          25          30
65 ata gag aat tac caa gga agg gat gcc act gat gcc ttc atg gtt atg      144
66 Ile Glu Asn Tyr Gln Gly Arg Asp Ala Thr Asp Ala Phe Met Val Met
68          35          40          45
70 cac tct caa gaa gcc ttc gac aag ctc aag cgc atg ccc aaa atc aat      192
71 His Ser Gln Glu Ala Phe Asp Lys Leu Lys Arg Met Pro Lys Ile Asn
72          50          55          60
74 ccc agt tct gag ttg cca ccc cag gct gca gtg aat gaa gct caa gag      240
75 Pro Ser Ser Glu Leu Pro Pro Gln Ala Ala Val Asn Glu Ala Gln Glu
76 65          70          75          80
78 gat ttc cgg aag ctc cga gaa gag ttg atc gca act ggc atg ttt gat      288
79 Asp Phe Arg Lys Leu Arg Glu Glu Leu Ile Ala Thr Gly Met Phe Asp
80          85          90          95
82 gcc tcc ccc ctc tgg tac tca tac aaa atc agc acc aca ctg ggc ctt      336
83 Ala Ser Pro Leu Trp Tyr Ser Tyr Lys Ile Ser Thr Thr Leu Gly Leu
84          100          105          110
86 gga gtg ctg ggt tat ttc ctg atg gtt cag tat cag atg tat ttc att      384
87 Gly Val Leu Gly Tyr Phe Leu Met Val Gln Tyr Gln Met Tyr Phe Ile
88          115          120          125
90 ggg gca gtg ttg ctt ggg atg cac tat caa cag atg ggc tgg ctt tct      432
91 Gly Ala Val Leu Leu Gly Met His Tyr Gln Gln Met Gly Trp Leu Ser
92          130          135          140
94 cat gac att tgc cac cac cag act ttc aag aac cgg aac tgg aac aac      480
95 His Asp Ile Cys His His Gln Thr Phe Lys Asn Arg Asn Trp Asn Asn
96 145          150          155          160
98 ctc gtg gga ctg gta ttt ggc aat ggt ctg caa ggt ttt tcc gtg aca      528
99 Leu Val Gly Leu Val Phe Gly Asn Gly Leu Gln Gly Phe Ser Val Thr
101          165          170          175
103 tgc tgg aag gac aga cac aat gca cat cat tcg gca acc aat gtt caa      576
104 Cys Trp Lys Asp Arg His Asn Ala His His Ser Ala Thr Asn Val Gln
105          180          185          190
107 ggg cac gac cct gat att gac aac ctc ccc ctc tta gcc tgg tct gag      624
108 Gly His Asp Pro Asp Ile Asp Asn Leu Pro Leu Leu Ala Trp Ser Glu
109          195          200          205
111 gat gac gtc aca cgg gcg tca ccg att tcc cgc aag ctc att cag ttc      672
112 Asp Asp Val Thr Arg Ala Ser Pro Ile Ser Arg Lys Leu Ile Gln Phe
113          210          215          220
115 cag cag tat tat ttc ttg gtc atc tgt atc ttg ttg cgg ttc att tgg      720
116 Gln Gln Tyr Tyr Phe Leu Val Ile Cys Ile Leu Leu Arg Phe Ile Trp
117 225          230          235          240
119 tgt ttc cag agc gtg ttg acc gtg cgc agt ctg aag gac aga gat aac      768
120 Cys Phe Gln Ser Val Leu Thr Val Arg Ser Leu Lys Asp Arg Asp Asn
121          245          250          255
123 caa ttc tat cgc tct cag tat aag aag gag gcc att ggc ctc gcc ctg      816
124 Gln Phe Tyr Arg Ser Gln Tyr Lys Lys Glu Ala Ile Gly Leu Ala Leu
125          260          265          270

```

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127 cat tgg aca ttg aag gcc ctg ttc cac tta ttc ttt atg ccc agc atc      864
128 His Trp Thr Leu Lys Ala Leu Phe His Leu Phe Phe Met Pro Ser Ile
129      275      280      285
131 ctc aca tcg ctg ttg gta ttt ttc gtt tcg gag ctg gtt ggc ggc ttc      912
132 Leu Thr Ser Leu Leu Val Phe Phe Val Ser Glu Leu Val Gly Gly Phe
135      290      295      300
137 ggc att gcg atc gtg gtg ttc atg aac cac tac cca ctg gag aag atc      960
138 Gly Ile Ala Ile Val Val Phe Met Asn His Tyr Pro Leu Glu Lys Ile
139 305      310      315      320
141 ggg gac tcg gtc tgg gat ggc cat gga ttc tcg gtt ggc cag atc cat      1008
142 Gly Asp Ser Val Trp Asp Gly His Gly Phe Ser Val Gly Gln Ile His
143      325      330      335
145 gag acc atg aac att cgg cga ggg att atc aca gat tgg ttt ttc gga      1056
146 Glu Thr Met Asn Ile Arg Arg Gly Ile Ile Thr Asp Trp Phe Phe Gly
147      340      345      350
149 ggc ttg aac tac cag atc gag cac cat ttg tgg ccg acc ctc cct cgc      1104
150 Gly Leu Asn Tyr Gln Ile Glu His His Leu Trp Pro Thr Leu Pro Arg
151      355      360      365
153 cac aac ctg aca gcg gtt agc tac cag gtg gaa cag ctg tgc cag aag      1152
154 His Asn Leu Thr Ala Val Ser Tyr Gln Val Glu Gln Leu Cys Gln Lys
155      370      375      380
157 cac aac ctg ccg tat cgg aac ccg ctg ccc cat gaa ggg ttg gtc atc      1200
158 His Asn Leu Pro Tyr Arg Asn Pro Leu Pro His Glu Gly Leu Val Ile
159 385      390      395      400
161 ctg ctg cgc tat ctg gcg gtg ttc gcc cgg atg gcg gag aag caa ccc      1248
162 Leu Leu Arg Tyr Leu Ala Val Phe Ala Arg Met Ala Glu Lys Gln Pro
163      405      410      415
165 gcg ggg aag gct cta taa      1266
166 Ala Gly Lys Ala Leu
168      420
171 <210> SEQ ID NO: 2
172 <211> LENGTH: 421
173 <212> TYPE: PRT
174 <213> ORGANISM: Euglena gracilis
176 <400> SEQUENCE: 2
178 Met Lys Ser Lys Arg Gln Ala Leu Pro Leu Thr Ile Asp Gly Thr Thr
179 1      5      10      15
182 Tyr Asp Val Ser Ala Trp Val Asn Phe His Pro Gly Gly Ala Glu Ile
183      20      25      30
186 Ile Glu Asn Tyr Gln Gly Arg Asp Ala Thr Asp Ala Phe Met Val Met
187      35      40      45
190 His Ser Gln Glu Ala Phe Asp Lys Leu Lys Arg Met Pro Lys Ile Asn
191      50      55      60
194 Pro Ser Ser Glu Leu Pro Gln Ala Ala Val Asn Glu Ala Gln Glu
195 65      70      75      80
198 Asp Phe Arg Lys Leu Arg Glu Glu Leu Ile Ala Thr Gly Met Phe Asp
199      85      90      95
202 Ala Ser Pro Leu Trp Tyr Ser Tyr Lys Ile Ser Thr Thr Leu Gly Leu
203      100      105      110

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Input Set : F:\Sequence listing (12810-00193-US).txt

Output Set: N:\CRF4\02142006\J566944.raw

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206 Gly Val Leu Gly Tyr Phe Leu Met Val Gln Tyr Gln Met Tyr Phe Ile
207          115          120          125
210 Gly Ala Val Leu Leu Gly Met His Tyr Gln Gln Met Gly Trp Leu Ser
211      130          135          140
214 His Asp Ile Cys His His Gln Thr Phe Lys Asn Arg Asn Trp Asn Asn
215 145          150          155          160
218 Leu Val Gly Leu Val Phe Gly Asn Gly Leu Gln Gly Phe Ser Val Thr
219          165          170          175
222 Cys Trp Lys Asp Arg His Asn Ala His His Ser Ala Thr Asn Val Gln
223          180          185          190
226 Gly His Asp Pro Asp Ile Asp Asn Leu Pro Leu Leu Ala Trp Ser Glu
227      195          200          205
230 Asp Asp Val Thr Arg Ala Ser Pro Ile Ser Arg Lys Leu Ile Gln Phe
231      210          215          220
234 Gln Gln Tyr Tyr Phe Leu Val Ile Cys Ile Leu Leu Arg Phe Ile Trp
235 225          230          235          240
238 Cys Phe Gln Ser Val Leu Thr Val Arg Ser Leu Lys Asp Arg Asp Asn
239          245          250          255
242 Gln Phe Tyr Arg Ser Gln Tyr Lys Lys Glu Ala Ile Gly Leu Ala Leu
243          260          265          270
246 His Trp Thr Leu Lys Ala Leu Phe His Leu Phe Phe Met Pro Ser Ile
247          275          280          285
250 Leu Thr Ser Leu Leu Val Phe Phe Val Ser Glu Leu Val Gly Gly Phe
251      290          295          300
254 Gly Ile Ala Ile Val Val Phe Met Asn His Tyr Pro Leu Glu Lys Ile
255 305          310          315          320
258 Gly Asp Ser Val Trp Asp Gly His Gly Phe Ser Val Gly Gln Ile His
259          325          330          335
262 Glu Thr Met Asn Ile Arg Arg Gly Ile Ile Thr Asp Trp Phe Phe Gly
263          340          345          350
266 Gly Leu Asn Tyr Gln Ile Glu His His Leu Trp Pro Thr Leu Pro Arg
267      355          360          365
270 His Asn Leu Thr Ala Val Ser Tyr Gln Val Glu Gln Leu Cys Gln Lys
271      370          375          380
274 His Asn Leu Pro Tyr Arg Asn Pro Leu Pro His Glu Gly Leu Val Ile
275 385          390          395          400
278 Leu Leu Arg Tyr Leu Ala Val Phe Ala Arg Met Ala Glu Lys Gln Pro
279          405          410          415
282 Ala Gly Lys Ala Leu
283          420
286 <210> SEQ ID NO: 3
287 <211> LENGTH: 777
288 <212> TYPE: DNA
289 <213> ORGANISM: Isochrysis galbana
291 <220> FEATURE:
292 <221> NAME/KEY: CDS
293 <222> LOCATION: (1)..(777)
294 <223> OTHER INFORMATION: delta9-elongase
296 <400> SEQUENCE: 3

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RAW SEQUENCE LISTING

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TIME: 12:55:17

Input Set : F:\Sequence listing (12810-00193-US).txt

Output Set: N:\CRF4\02142006\J566944.raw

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297 atg gcc ctc gca aac gac gcg gga gag cgc atc tgg gcg gct gtg acc      48
298 Met Ala Leu Ala Asn Asp Ala Gly Glu Arg Ile Trp Ala Ala Val Thr
299 1          5          10          15
301 gac ccg gaa atc ctc att ggc acc ttc tcg tac ttg cta ctc aaa ccg      96
302 Asp Pro Glu Ile Leu Ile Gly Thr Phe Ser Tyr Leu Leu Leu Lys Pro
303          20          25          30
305 ctg ctc cgc aat tcc ggg ctg gtg gat gag aag aag ggc gca tac agg      144
306 Leu Leu Arg Asn Ser Gly Leu Val Asp Glu Lys Lys Gly Ala Tyr Arg
307          35          40          45
309 acg tcc atg atc tgg tac aac gtt ctg ctg gcg ctc ttc tct gcg ctg      192
310 Thr Ser Met Ile Trp Tyr Asn Val Leu Leu Ala Leu Phe Ser Ala Leu
311          50          55          60
313 agc ttc tac gtg acg gcg acc gcc ctc ggc tgg gac tat ggt acg ggc      240
314 Ser Phe Tyr Val Thr Ala Thr Ala Leu Gly Trp Asp Tyr Gly Thr Gly
315 65          70          75          80
317 gcg tgg ctg cgc agg caa acc ggc gac aca ccg cag ccg ctc ttc cag      288
318 Ala Trp Leu Arg Arg Gln Thr Gly Asp Thr Pro Gln Pro Leu Phe Gln
319          85          90          95
321 tgc ccg tcc ccg gtt tgg gac tcg aag ctc ttc aca tgg acc gcc aag      336
322 Cys Pro Ser Pro Val Trp Asp Ser Lys Leu Phe Thr Trp Thr Ala Lys
323          100          105          110
325 gca ttc tat tac tcc aag tac gtg gag tac ctc gac acg gcc tgg ctg      384
326 Ala Phe Tyr Tyr Ser Lys Tyr Val Glu Tyr Leu Asp Thr Ala Trp Leu
327          115          120          125
329 agg gtc tcc ttt ctc cag gcc ttc cac cac ttt ggc gcg ccg tgg gat      432
330 Arg Val Ser Phe Leu Gln Ala Phe His His Phe Gly Ala Pro Trp Asp
331          130          135          140
333 gtg tac ctc ggc att cgg ctg cac aac gag ggc gta tgg atc ttc atg      480
334 Val Tyr Leu Gly Ile Arg Leu His Asn Glu Gly Val Trp Ile Phe Met
335 145          150          155          160
337 ttt ttc aac tcg ttc att cac acc atc atg tac acc tac tac ggc ctc      528
338 Phe Phe Asn Ser Phe Ile His Thr Ile Met Tyr Thr Tyr Tyr Gly Leu
339          165          170          175
341 acc gcc gcc ggg tat aag ttc aag gcc aag ccg ctc atc acc gcg atg      576
342 Thr Ala Ala Gly Tyr Lys Phe Lys Ala Lys Pro Leu Ile Thr Ala Met
343          180          185          190
345 cag atc tgc cag ttc gtg ggc ggc ttc ctg ttg gtc tgg gac tac atc      624
346 Gln Ile Cys Gln Phe Val Gly Gly Phe Leu Leu Val Trp Asp Tyr Ile
347          195          200          205
349 aac gtc ccc tgc ttc aac tcg gac aaa ggg aag ttg ttc agc tgg gct      672
350 Asn Val Pro Cys Phe Asn Ser Asp Lys Gly Lys Leu Phe Ser Trp Ala
351          210          215          220
353 ttc aac tat gca tac gtc ggc tcg gtc ttc ttg ctc ttc tgc cac ttt      720
354 Phe Asn Tyr Ala Tyr Val Gly Ser Val Phe Leu Leu Phe Cys His Phe
355 225          230          235          240
357 ttc tac cag gac aac ttg gca acg aag aaa tcg gcc aag gcg ggc aag      768
358 Phe Tyr Gln Asp Asn Leu Ala Thr Lys Lys Ser Ala Lys Ala Gly Lys
359          245          250          255
361 cag ctc tag      777

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<210> SEQ ID NO 115
 <211> LENGTH: 13
 <212> TYPE: PRT
 <213> ORGANISM: Unknown
 <220> FEATURE:

<221> NAME/KEY: MISC_FEATURE
 <222> LOCATION: (1)..(13)

<223> OTHER INFORMATION: Xaa in the sequence at position 2, 3, 4, 6, 7, 8 and 9 has the meaning given in Table A.

<220> FEATURE:

<221> NAME/KEY: MISC_FEATURE
 <222> LOCATION: (1)..(13)

<223> OTHER INFORMATION: Consensus
 <400> SEQUENCE: 115

Asn Xaa Xaa Xaa His Xaa Xaa Met Tyr Xaa Tyr Tyr Xaa
 1 5 10

Tyr at this
 Location

Invalid Response. Xaa¹ Represents
 Single Amino Acid. P/s see Item
 #9 in Error
 Summary Sheet.

F41

The type of errors shown exist throughout
 the Sequence Listing. Please check subsequent
 sequences for similar errors.

RAW SEQUENCE LISTING ERROR SUMMARY

DATE: 02/14/2006

PATENT APPLICATION: US/10/566,944

TIME: 12:55:18

Input Set : F:\Sequence listing (12810-00193-US).txt

Output Set: N:\CRF4\02142006\J566944.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:115; Xaa Pos. 2,3,4,6,7,10,13

Seq#:116; Xaa Pos. 3,4,5,6

Seq#:139; Xaa Pos. 3,4

Seq#:140; Xaa Pos. 2,3,5,6

Seq#:141; Xaa Pos. 3

Seq#:142; Xaa Pos. 5,6

Seq#:185; N Pos. 3,18

Seq#:186; N Pos. 3,9,12,15,21

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:115; Line(s) 12392

Seq#:116; Line(s) 12415

Seq#:140; Line(s) 13593

Seq#:142; Line(s) 13635

VERIFICATION SUMMARY

DATE: 02/14/2006

PATENT APPLICATION: US/10/566,944

TIME: 12:55:18

Input Set : F:\Sequence listing (12810-00193-US).txt

Output Set: N:\CRF4\02142006\J566944.raw

L:20 M:270 C: Current Application Number differs, Replaced Current Application No
L:20 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:12403 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:115 after pos.:0
L:12426 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:116 after pos.:0
L:13581 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:139 after pos.:0
L:13602 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:140 after pos.:0
L:13623 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:141 after pos.:0
L:13646 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:142 after pos.:0
L:14407 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:185 after pos.:0
L:14426 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:186 after pos.:0